

Fig. 1

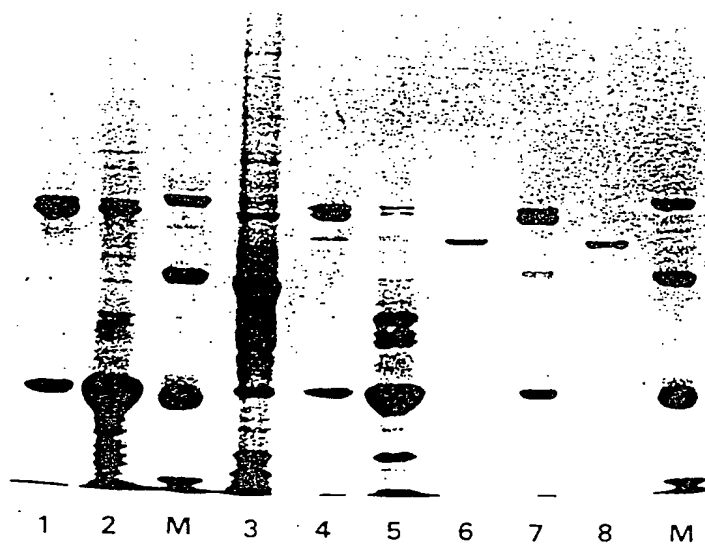


Fig. 2

adseverin C39	KVAHVKQIPFDA
gelsolin	³⁸⁶ HIANVERVPFDA
villin	³⁶⁵ KVAKVEQVKFDA

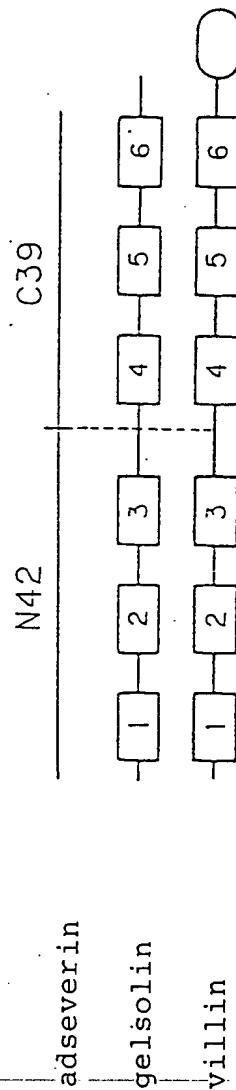


Fig. 3

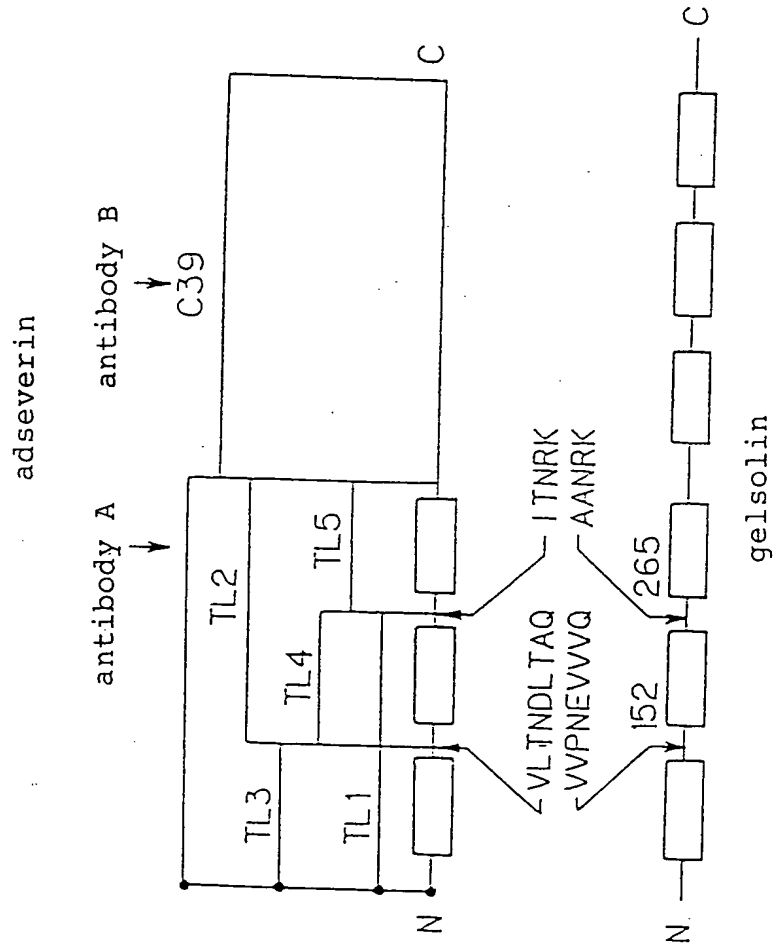


Fig. 4

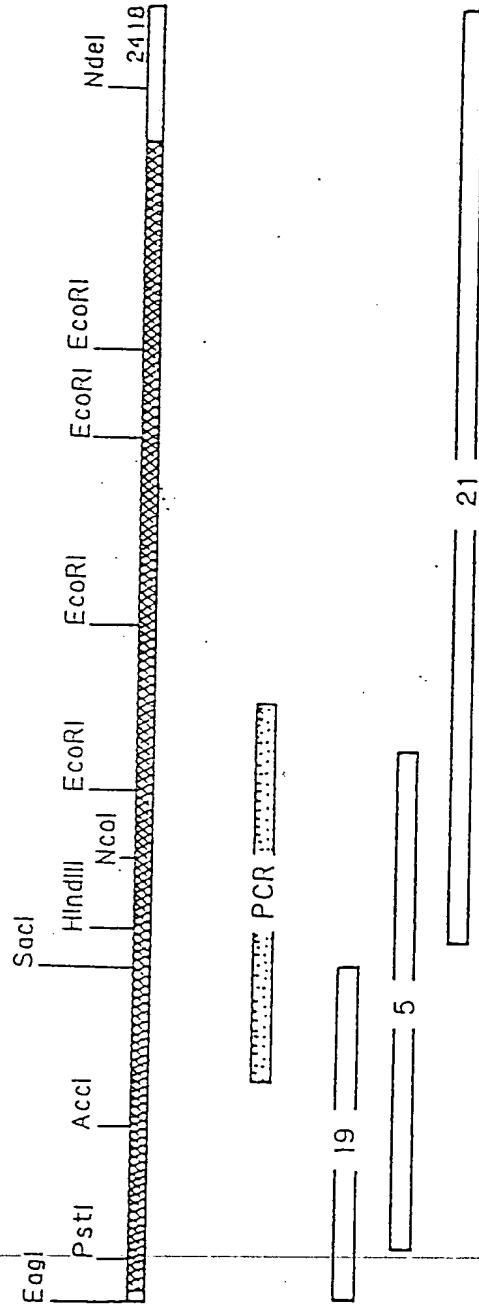


Fig. 5A

ADS	008	EEFAR-AGK-R	AGLQVWRIE	KLELVVPESAYGN	1
GEL	057	PEFLK-AGK-E	PGLQIWRIE	KEDLVVPPTNL YGD	
VIL	007	QVKGS-INITT	PGLQIWRIE	AMQMVPPSPSTFGS	
ADS	385	AAQHHVVDDGS	GKVQIWRIE	NGRVEIDRNSYGE	
GEL	434	AAQHGMDDDGT	GQKQIWRIE	GSNKVPVDPATYGQ	4
VIL	387	AAQQKMVDDGS	GEVQVWRIE	NLELVVDSKWLGH	
ADS	127	NHVLTNDLTAQ	RLLHVKGR	-VVRATEVPLSWDS	
GEL	177	KHVPNEVVVQ	RLFQVKGR	-VVRATEVPSWES	2
VIL	127	KHVEITNSYDVQ	RLLHVKGR	NVV-AGEVEMSWKS	
ADS	503	GQAPAPI--RL	FQVRRNLAS	ITRIM-EVDVDANS	
GEL	556	GQTAPAST--RL	FQVRANSAG	ATRAV-EVLPRKAGA	5
VIL	508	NLETGPST--RL	FQVQGTGAN	NTKAF-EVPARANF	
ADS	245	NRKMAK-LYMV	SDASGSMKV	SLVAEENPFMAM	
GEL	294	NRKLAK-LYKV	SNGAGTMSV	SLVADENPFAQGA	3
VIL	250	KAAL-K-LYHV	SDSEGNLVV	REVAT-RPLTQDL	
ADS	610	ED-HPRLYGC	SNKTGRFII	EEVPGE--FTQDD	
GEL	662	MDAHPRLFAC	SNKIGRFVI	EEVPGE--LMQED	6
VIL	615	LVI-TPRLFEC	SNKTGRFLA	TEIP-D--FNQDD	

Fig. 5B

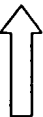

ADS	F	YVG	D	A	YLV	LHTTQASRG---FTYR	L	HF	W	L	G	KECTQD	E	STA	A	1
GEL	F	FTG	D	A	YVI	LKTVQLRNGN--LQYD	L	HY	W	L	G	NECSQD	E	SGA	A	
VIL	F	FDG	D	C	YII	LAIH--KTASS-LSYD	I	HY	W	I	G	QDSSLD	E	QGA	A	
ADS	F	YGG	D	C	YII	LYTYPR---GQI---	I	YT	W	Q	G	ANATRD	E	LTT	S	4
GEL	F	YGG	D	S	YII	LYNYRHGGRQGQI---	I	YN	W	Q	G	AQSTQD	E	VAA	S	
VIL	F	YGG	D	C	YLL	LYTYLIGEKQHYL----	L	YV	W	Q	G	SQASQD	E	ITA	S	
ADS	F	NKG	D	C	FII	-----DLGTE	I	YQ	W	C	G	SSCNKY	E	RLK	A	2
GEL	F	NNG	D	C	FII	-----DLGNN	I	HQ	W	C	G	SNSNRY	E	RLK	A	
VIL	F	NRG	D	V	FLL	-----DLGKL	I	IQ	W	N	G	PESTRM	E	RLR	G	
ADS	L	NSN	D	V	FVL	-----KLRQNN	G	YI	W	I	G	KGSTQE	E	EKG	A	5
GEL	L	NSN	D	A	FVL	-----KT-PSA	A	YL	W	V	G	TGASEA	E	KTG	A	
VIL	L	NSN	D	V	FVL	-----KT-QSC	C	YL	W	C	G	KGCSCD	E	REM	A	
ADS	L	LSE	E	C	FII	-----DHGAQKQ	I	FV	W	K	G	KDANPQ	E	RKA	A	3
GEL	L	KSE	D	C	FII	-----DHGKDGK	I	FV	W	K	G	KQANTE	E	RKA	A	
VIL	L	SHE	D	C	YII	-----DQG-GLK	I	YV	W	K	G	KKANEQ	E	KKG	A	
ADS	L	AED	D	V	MLL	-----DAWEQ	I	FI	W	I	G	KDANEV	E	KSE	S	6
GEL	L	ATD	D	V	MLL	-----DTWDQ	V	FV	W	V	G	KDSQEE	E	KTE	A	
VIL	L	EED	D	V	FLL	-----DVWDQ	V	FF	W	I	G	KHANEV	E	KKA	A	

← Motif B →

← Motif A →

Fig. 5C

ADS	AIFTVQMDDYLGKPVQNRREL-----	QG	Y	ES	TD	FV	G	YF
GEL	AIFTVQLDYLNRAVQHREV-----	QG	F	ES	AT	FL	G	YF
VIL	AIYTTQMDDFLKGRAVQHREV-----	QG	N	ES	EA	FR	G	YF
ADS	AFLTVQLDRSLGGQAVQIRVS-----	QG	K	EP	AH	LL	S	LF
GEL	AILTAQLDELGGTPVQSRVV-----	QG	K	EP	AH	LM	S	LF
VIL	AYQAVILDQKYNGEPVQIRVP-----	MG	K	EP	PH	LM	S	IF
ADS	SQVAIGIRDNERKGRAQLIVE----	EG	S	EP	SE	LT	K	VL
GEL	TQVSKGIRDNERSGRARVHVSE----	EG	T	EP	EA	ML	Q	VL
VIL	MTLAKEIRDQERGGRITYGVVDGEN	EL	A	SP	-K	LM	E	VM
ADS	EYVASVL-----KCKTSTIQ-----	EG	K	EP	EE	FW	N	SL
GEL	QELLRLV-----RAQPVQVA-----	EG	S	EP	DG	FW	E	AL
VIL	KMVADTISRTEK-----QV-VV-----	EG	Q	EP	AN	FW	M	AL
ADS	MKTAEFFLQOMNYSTNT-QIQVLP-	EG	G	ET	P	IF	KQ	FF
GEL	LKTASDFITKMDYPKQT-QVSVLP-	EG	G	ET	P	LF	KQ	FF
VIL	MSHALNFIKAKQYPPST-QVEVQN-	DG	A	ES	A	VF	QQ	LF
ADS	LKSAKIYLETDPGGRDKRTPIVIIL	QG	H	EP	PT	FT	GW	FL
GEL	LTSAKRYIETDPANRDRRTPITVK	QG	F	EP	PS	FV	GW	FL
VIL	ATTAQOEYLTHTPSGRDPETPIIVK	QG	H	EP	PT	FT	GW	FL

 Motif C 

6

3

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2

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1

Fig. 5D

ADS	-	KGGLKY---KA	GGVASGL	126	
GEL	-	KSGLKY---KK	GGVASGF	176	1
VIL	-	KQGLVI---RK	GGVASGM	126	
ADS	-	KDKPLI IY	KNGTSKKE	502	
GEL	-	GGKPMI IY	KGGSREG	555	4
VIL	-	KGR-MV VY	QGGTSRTN	507	
ADS	-	GEKPKLRD	GEDDDIKADIT	244	
GEL	-	GPKPALPA	GTEDTA-KEDAA	293	2
VIL	N	HVLGKRRELKA	AVPDTV-VEPAL	249	
ADS	-	GGK---KD	YQTS-PLLESQA	609	
GEL	-	GGK---AA	YRTS-PLKDKK	661	5
VIL	-	GGK---AP	YANT-KRLQ EEN	614	
ADS	K	DWRDRDQSDGF	GKVVYTEKVAH	367	
GEL	K	NWRDPDQTDGL	GLSYLSSHIAN	416	3
VIL	Q	KWTASNRTSGL	GKTHTVGSVAK	369	
ADS	G	WDSSRW		715	
GEL	G	WDDDYWSVDPL	-DRAMAELAA	782	
VIL	A	WDPFKWSN TKS	YEDLKAESGN	734	6



Fig. 5E



Fig. 6

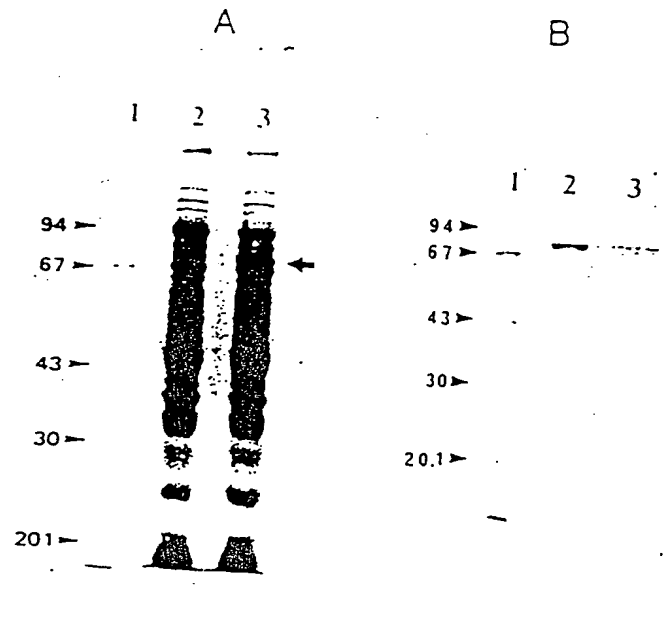
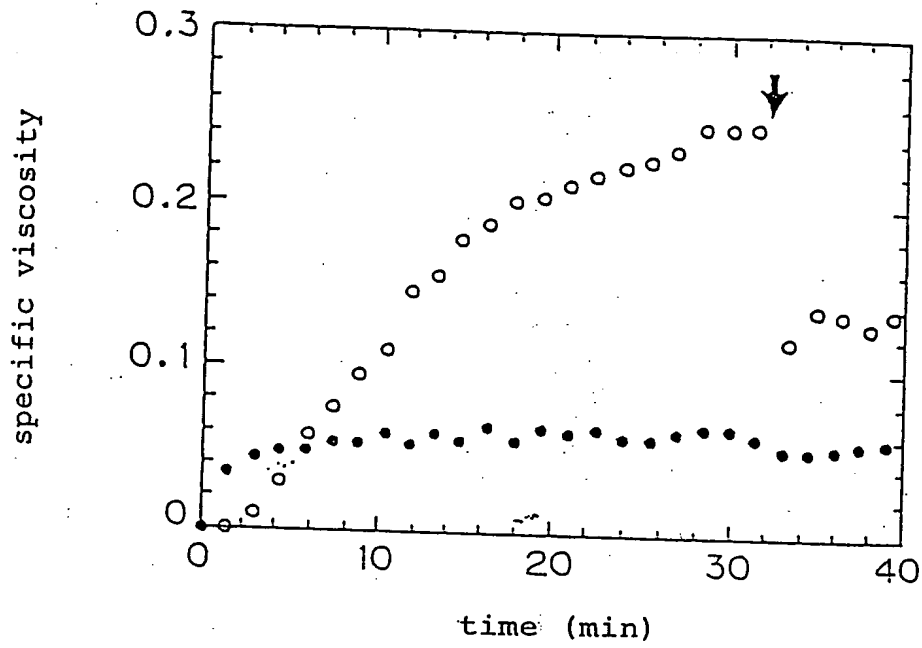


Fig. 7

A



B

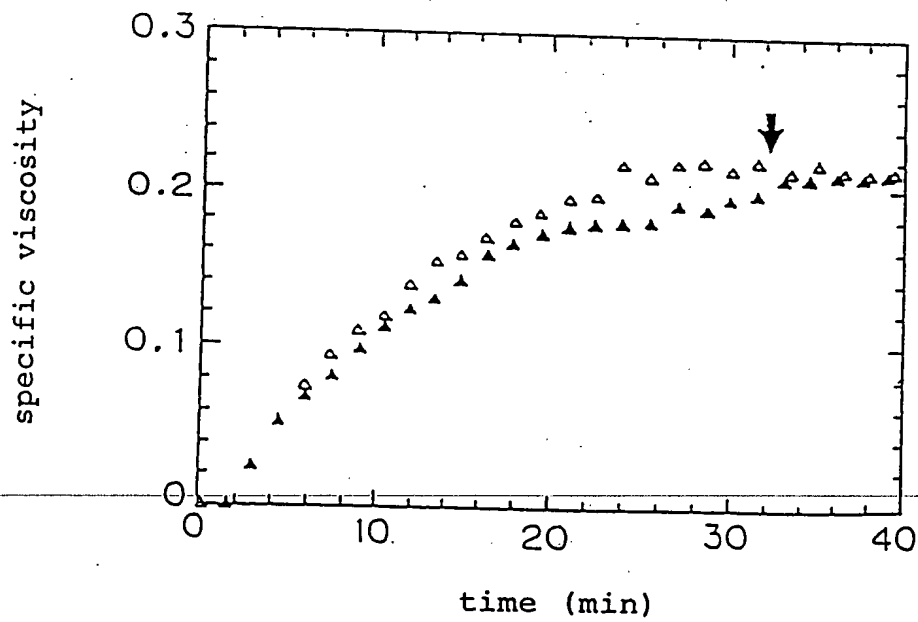


Fig. 8

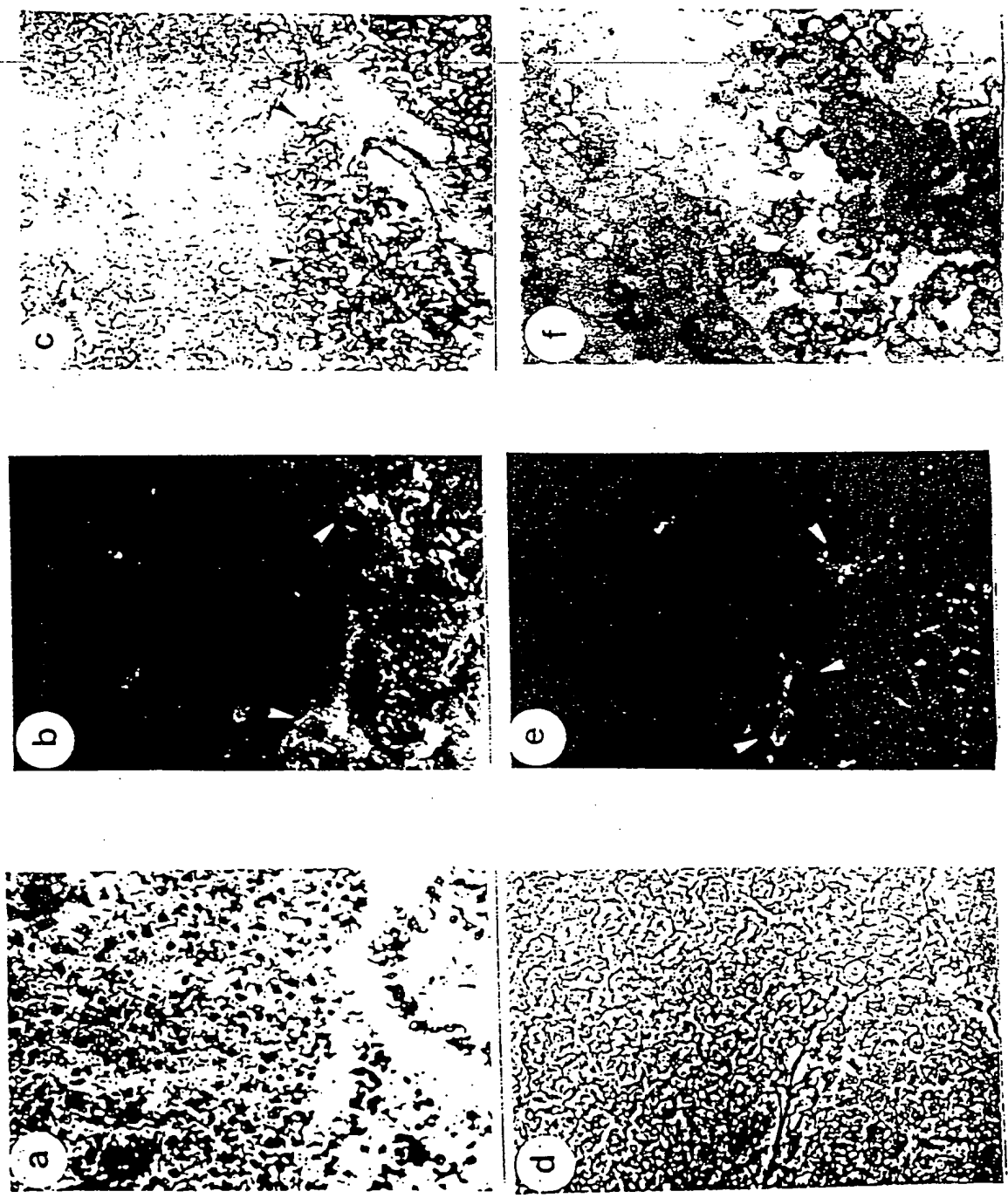


Fig. 9

1' MARELYHEEFARAGKQAGLQVWRIEXLELYPVPSAHGDFYVGDAYLVLHTAKTSRGFTY

 1" MAOGLYHEEFARAGKRAGLQVWRIEXLELYVPESAYGNFYVGDAYLVLHTTQASRGFTY

 61' HLHFWLGKECSQDESTAAAIFTVQMDOYLGGKPVQNRRELQGYESNDFVSYFKGGLKYKAG

 61" RLHFWLGKECTQDESTAAAIFTVQMDOYLGGKPVQNRRELQGYESTDFVGYFKGGLKYKAG

 121' GVASGLNHVLTNDLTAKRLLVHKGRVVRATEVPLSWDSFNKGDCFIIDLGTETIYQWCGS

 121" GVASGLNHVLTNDLTACRLLVHKGRVVRATEVPLSWDSFNKGDCFIIDLGTETIYQWCGS

 181' SCNKYERLKANQVATGIRYNERKGRSELIWVEEGSEPSSELIKVLGEKPELPOGGDDDDII

 181" SCNKYERLKASQVAIGIRDNERKGRAQLIWVEEGSEPSSELTAKVLGEKPKLRDGEDDDDDIK

 241' ADISNRKMAKLYMVSDASGSMRVTVVAEENPFMSMALLSEECFILDHGAAKQIFVWKGKD

 241" ADITNRKMAKLYMVSDASGSMKVSVAEENPFMSMALLSEECFILDHGAAKQIFVWKGKD

 301' ANPQERKAAMKTAEEFLQQMNYSTNTQIQVLPEGGETPIFKQFFKDWRDKDQSDGFGKVV

 301" ANPQERKAAMKTAEEFLQQMNYSTNTQIQVLPEGGETPIFKQFFKDWRDRDQSDGFGKVV

 361' VTEKVAQIKQIPFDASKLHSSPQMAAQHNMVDDGSGKVEIWRVENNNGRIQVDQNSYGEFY

 361" VTEKVAHVQKIPFDASKLHSSPQMAAQHHVDDGSGKVQIWRVENNNGRVEIDRNSYGEFY

 421' GGDCYIILYTYPRGQIIYTWQGANATRDELTTSAFLTQVQLDRSLGGQAVQIRVSQKPEV

 421" GGDCYIILYTYPRGQIIYTWQGANATRDELTTSAFLTQVQLDRSLGGQAVQIRVSQKKEPA

 481' HLLSLFKDKPLIIYKNGTSKKGGQAPAPPTRLFQVRRNLASITRIVEVDVDANSLNSNDV

 481" HLLSLFKDKPLIIYKNGTSKKEGQAPAPPIRLFQVRRNLASITRIMEVDVDANSLNSNDV

 541' CVLKLQNSGYIWWGKGASQEEKGAEYVASVLKCKTLRIQEGEPEEFWNSLGKKDYQ

 541" FVLKLQNNGYIWWGKGSTQEEKGAEYVASVLKCKTSTIQEGKEPEEFWNSLGKKDYQ

 601' TSPLLTQAEDHPPRLYGCSNKTGRFVIEEIPGEFTQODLAEDOVMLLDAAEQIFIWIGK

 601" TSPLLSQAEDHPPRLYGCSNKTGRFIEEVPGEFTQODLAEDOVMLLDAAEQIFIWIGK

 661' DANEVEKKESLSAKMYLETDPGROKRTPIVVIKQGHEPPTFTGNFLGWSSKW

 661" DANEVEKSESLSAKIYLETDPGROKRTPIVVIKQGHEPPTFTGNFLGWSSRW